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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/045,400C

DATE: 06/06/2003

TIME: 08:03:09

Input Set : A:\P-CAN 1004 Sequence Listing.txt
Output Set: N:\CRF4\06062003\J045400C.raw

3 <110> APPLICANT: Moon, Chulso
4 Mao, Li
6 <120> TITLE OF INVENTION: DAP-Kinase and HOXA9, Two Human Genes Associated with
Genesis,
7 Progression, and Aggressiveness of Non-Small Cell Lung Cancer
9 <130> FILE REFERENCE: 10620-1U1
11 <140> CURRENT APPLICATION NUMBER: 10/045,400C
12 <141> CURRENT FILING DATE: 2001-11-29
14 <150> PRIOR APPLICATION NUMBER: US 60/250,083
15 <151> PRIOR FILING DATE: 2000-11-29
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 20
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: HoxA9 PCR Primer
29 <400> SEQUENCE: 1
30 cccgccttat ggcattaaac 20
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 20
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial
38 <220> FEATURE:
39 <223> OTHER INFORMATION: HoxA9 PCR Primer
41 <400> SEQUENCE: 2
42 agttggctgc tgggttattg 20
45 <210> SEQ ID NO: 3
46 <211> LENGTH: 218
47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial
50 <220> FEATURE:
51 <223> OTHER INFORMATION: HoxA9 Probe
53 <400> SEQUENCE: 3
54 cccgccttat ggcattaaac ctgaaccgct gtcggccaga aggggtgact gtcccacgct 60
55 tgacactcac actttgtccc tgactgacta tgcttgggt ttcctccag ttgatagaga 120
58 aaaaacaaccc agcgaaggcg cttctccga aaacaatgcc gagaatgaga gcggcggaga 180
60 caagcccccc atcgatccca ataacccagc agccaact 218
63 <210> SEQ ID NO: 4
64 <211> LENGTH: 5910
65 <212> TYPE: DNA
66 <213> ORGANISM: Homo sapiens
68 <220> FEATURE:

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69 <221> NAME/KEY: CDS
 70 <222> LOCATION: (337)..(4632)
 71 <223> OTHER INFORMATION:

W--> 73 <400> 4

74	cgaggacag	ccggaccgag	ccaacgcgg	ggactttgtt	ccctccacgg	aggggactcg	60
76	gcaactcgca	gcggcagggt	ctggggccgg	cgcctggag	ggatctgcgc	ccccactca	120
78	ctccctagct	gtgttcccgc	cgcgcggcc	gctagtctcc	ggcgctggcg	cctatggtcg	180
80	gcctccgaca	gcccgtccgga	gggaccgggg	gagctccag	gcccgggg	ctggagactg	240
82	atgcatgagg	ggcctacgga	ggcgcaggag	cggtgggtat	ggtctggaa	gcggagctga	300
84	agtcccctgg	gcttttgta	ggcggtacag	tttatac	atg	acc	978
85					Met	Thr	
86						Val	
						Phe	
						Arg	
						Gln	
88	gaa aac	gtg gat	gat tac	tac gac	acc ggc	gag gaa	402
89	Glu	Asn	Val	Asp	Asp	Tyr	
90	10				15		
						20	
92	cag ttt	gct gtt	gtg aag	aaa tgc	cgt gag	aaa agt	450
93	Gln	Phe	Ala	Val	Val	Lys	
94	25				30		
						35	
96	tat gcc	gcc aaa	ttc atc	aag aaa	agg agg	act aag	498
97	Tyr	Ala	Ala	Lys	Phe	Ile	
98	40				45		
						50	
100	ggt gtg	agc cgc	gag gac	atc gag	cggtc	agc atc	546
101	Gly	Val	Ser	Arg	Glu	Asp	
102	55				60		
						65	
						70	
104	atc cag	cac ccc	aat gtc	atc acc	ctg cac	gag gtc	594
105	Ile	Gln	His	Pro	Asn	Val	
106	75				80		
						85	
108	acg gac	gtc atc	ctg atc	ttg gaa	ctc gtt	gca ggt	642
109	Thr	Asp	Val	Ile	Leu	Ile	
110	90				95		
						100	
112	gac ttc	tta gct	gaa aag	gaa tct	tta act	gaa gag	690
113	Asp	Phe	Leu	Ala	Glu	Ser	
114	105				110		
						115	
116	ttt ctc	aaa caa	att ctt	aat ggt	gtt tac	tac ctg	738
117	Phe	Leu	Lys	Gln	Ile	Leu	
118	120				125		
						130	
120	atc gcc	cac ttt	gat ctt	aag cct	gag aac	ata atg	786
121	Ile	Ala	His	Phe	Asp	Leu	
122	135				140		
						145	
							150
124	aat gtc	ccc aaa	cct cgg	atc aag	atc att	gac ttt	834
125	Asn	Val	Pro	Lys	Pro	Arg	
126	155				160		
						165	
128	aaa att	gac ttt	gga aat	gaa ttt	aaa aac	ata ttt	882
129	Lys	Ile	Asp	Phe	Gly	Asn	
130	170				175		
						180	
132	ttt gtc	gct cct	gag ata	gtc aac	tat gaa	cct ctt	930
133	Phe	Val	Ala	Pro	Glu	Ile	
134	185				190		
						195	
136	gat atg	tgg agt	atc ggg	gta ata	acc tat	atc ctc	978
						gtt gca	

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137	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	Tyr	Ile	Leu	Leu	Ser	Gly	Ala	
138	200				205						210						
140	tcc	cca	ttt	ctt	gga	gac	act	aag	caa	gaa	acg	tta	gca	aat	gta	tcc	1026
141	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	Glu	Thr	Leu	Ala	Asn	Val	Ser	
142	215				220				225			230					
144	gct	gtc	aac	tac	gaa	ttt	gag	gat	gaa	tac	ttc	agt	aat	acc	agt	gcc	1074
145	Ala	Val	Asn	Tyr	Glu	Phe	Glu	Asp	Glu	Tyr	Phe	Ser	Asn	Thr	Ser	Ala	
146					235				240			245					
148	cta	gcc	aaa	gat	ttc	ata	aga	aga	ctt	ctg	gtc	aag	gat	cca	aag	aag	1122
149	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Arg	Leu	Leu	Val	Lys	Asp	Pro	Lys	Lys	
150					250				255			260					
152	aga	atg	aca	att	caa	gat	agt	ttg	cag	cat	ccc	tgg	atc	aag	cct	aaa	1170
153	Arg	Met	Thr	Ile	Gln	Asp	Ser	Leu	Gln	His	Pro	Trp	Ile	Lys	Pro	Lys	
154					265				270			275					
156	gat	aca	caa	cag	gca	ctt	agt	aga	aaa	gca	tca	gca	gta	aac	atg	gag	1218
157	Asp	Thr	Gln	Gln	Ala	Leu	Ser	Arg	Lys	Ala	Ser	Ala	Val	Asn	Met	Glu	
158					280				285			290					
160	aaa	ttc	aag	aag	ttt	gca	gcc	cg	aaa	aaa	tgg	aaa	caa	tcc	gtt	cgc	1266
161	Lys	Phe	Lys	Lys	Phe	Ala	Ala	Arg	Lys	Lys	Trp	Lys	Gln	Ser	Val	Arg	
162					295				300			305			310		
164	ttg	ata	tca	ctg	tgc	caa	aga	tta	tcc	agg	tca	ttc	ctg	tcc	aga	agt	1314
165	Leu	Ile	Ser	Leu	Cys	Gln	Arg	Leu	Ser	Arg	Ser	Phe	Leu	Ser	Arg	Ser	
166					315				320			325					
168	aac	atg	agt	gtt	gcc	aga	agc	gat	gat	act	ctg	gat	gag	gaa	gac	tcc	1362
169	Asn	Met	Ser	Val	Ala	Arg	Ser	Asp	Asp	Thr	Leu	Asp	Glu	Glu	Asp	Ser	
170					330				335			340					
172	ttt	gtg	atg	aaa	gcc	atc	atc	cat	gcc	atc	aac	gat	gac	aat	gtc	cca	1410
173	Phe	Val	Met	Lys	Ala	Ile	Ile	His	Ala	Ile	Asn	Asp	Asp	Asn	Val	Pro	
174					345				350			355					
176	ggc	ctg	cag	cac	ctt	ctg	ggc	tca	tta	tcc	aac	tat	gat	gtt	aac	caa	1458
177	Gly	Leu	Gln	His	Leu	Leu	Gly	Ser	Leu	Ser	Asn	Tyr	Asp	Val	Asn	Gln	
178					360				365			370					
180	ccc	aac	aag	cac	ggg	aca	cct	cca	tta	ctc	att	gct	gct	tgt	ggg		1506
181	Pro	Asn	Lys	His	Gly	Thr	Pro	Pro	Leu	Leu	Ile	Ala	Ala	Gly	Cys	Gly	
182					375				380			385			390		
184	aat	att	caa	ata	cta	cag	ttg	ctc	att	aaa	aga	ggc	tcg	aga	atc	gat	1554
185	Asn	Ile	Gln	Ile	Leu	Gln	Leu	Leu	Ile	Lys	Arg	Gly	Ser	Arg	Ile	Asp	
186					395				400			405					
188	gtc	cag	gat	aag	ggc	ggg	tcc	aat	gcc	gtc	tac	tgg	gct	gct	cgg	cat	1602
189	Val	Gln	Asp	Lys	Gly	Gly	Ser	Asn	Ala	Val	Tyr	Trp	Ala	Ala	Arg	His	
190					410				415			420					
192	ggc	cac	gtc	gat	acc	ttg	aaa	ttt	ctc	agt	gag	aac	aaa	tgc	cct	ttg	1650
193	Gly	His	Val	Asp	Thr	Leu	Lys	Phe	Leu	Ser	Glu	Asn	Lys	Cys	Pro	Leu	
194					425				430			435					
196	gat	gtg	aaa	gac	aag	tct	gga	gag	atg	gcc	ctc	cac	gtg	gca	gct	cgc	1698
197	Asp	Val	Lys	Asp	Lys	Ser	Gly	Glu	Met	Ala	Leu	His	Val	Ala	Ala	Arg	
198					440				445			450					
200	tat	ggc	cat	gct	gac	gtg	gct	caa	gtt	act	tgt	gca	gct	tcg	gct	caa	1746
201	Tyr	Gly	His	Ala	Asp	Val	Ala	Gln	Val	Thr	Cys	Ala	Ala	Ser	Ala	Gln	

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202	455	460	465	470	
204	atc cca ata tcc agg aca aag gaa gaa acc ccc ctg cac tgt gct				1794
205	Ile Pro Ile Ser Arg Thr Lys Glu Glu Glu Thr Pro Leu His Cys Ala				
206	475	480	485		
208	gct tgg cac ggc tat tac tct gtg gcc aaa gcc ctt tgt gaa gcc ggc				1842
209	Ala Trp His Gly Tyr Tyr Ser Val Ala Lys Ala Leu Cys Glu Ala Gly				
210	490	495	500		
212	tgt aac gtg aac atc aag aac cga gaa gga gag acg ccc ctc ctg aca				1890
213	Cys Asn Val Asn Ile Lys Asn Arg Glu Gly Glu Thr Pro Leu Leu Thr				
214	505	510	515		
216	gcc tct gcc agg ggc tac cac gac atc gtg gag tgt ctg gcc gaa cat				1938
217	Ala Ser Ala Arg Gly Tyr His Asp Ile Val Glu Cys Leu Ala Glu His				
218	520	525	530		
220	gga gcc gac ctt aat gct tgc gac aag gac gga cac att gcc ctt cat				1986
221	Gly Ala Asp Leu Asn Ala Cys Asp Lys Asp Gly His Ile Ala Leu His				
222	535	540	545	550	
224	ctg gct gta aga cgg tgt cag atg gag gta atc aag act ctc ctc agc				2034
225	Leu Ala Val Arg Arg Cys Gln Met Glu Val Ile Lys Thr Leu Leu Ser				
226	555	560	565		
228	caa ggg tgt ttc gtc gat tat caa gac agg cac ggc aat act ccc ctc				2082
229	Gln Gly Cys Phe Val Asp Tyr Gln Asp Arg His Gly Asn Thr Pro Leu				
230	570	575	580		
232	cat gtg gca tgt aaa gat ggc aac atg cct atc gtg gtg gcc ctc tgt				2130
233	His Val Ala Cys Lys Asp Gly Asn Met Pro Ile Val Val Ala Leu Cys				
234	585	590	595		
236	gaa gca aac tgc aat ttg gac atc tcc aac aag tat ggg cga acg cct				2178
237	Glu Ala Asn Cys Asn Leu Asp Ile Ser Asn Lys Tyr Gly Arg Thr Pro				
238	600	605	610		
240	ctg cac ctt gcg gcc aac aac gga atc cta gac gtg gtc cgg tat ctc				2226
241	Leu His Leu Ala Ala Asn Asn Gly Ile Leu Asp Val Val Arg Tyr Leu				
242	615	620	625	630	
244	tgt ctg atg gga gcc agc gtt gag gcg ctg acc acg gac gga aag acg				2274
245	Cys Leu Met Gly Ala Ser Val Glu Ala Leu Thr Thr Asp Gly Lys Thr				
246	635	640	645		
248	gca gaa gat ctt gct aga tcg gaa cag cac gag cac gta gca ggt ctc				2322
249	Ala Glu Asp Leu Ala Arg Ser Glu Gln His Glu His Val Ala Gly Leu				
250	650	655	660		
252	ctt gca aga ctt cga aag gat acg cac cga gga ctc ttc atc cag cag				2370
253	Leu Ala Arg Leu Arg Lys Asp Thr His Arg Gly Leu Phe Ile Gln Gln				
254	665	670	675		
256	ctc cga ccc aca cag aac ctg cag cca aga att aag ctc aag ctg ttt				2418
257	Leu Arg Pro Thr Gln Asn Leu Gln Pro Arg Ile Lys Leu Lys Leu Phe				
258	680	685	690		
260	ggc cac tcg gga tcc ggg aaa acc acc ctt gta gaa tct ctc aag tgt				2466
261	Gly His Ser Gly Ser Gly Lys Thr Thr Leu Val Glu Ser Leu Lys Cys				
262	695	700	705	710	
264	ggg ctg ctg agg agc ttt ttc aga agg cgt cgg ccc aga ctg tct tcc				2514
265	Gly Leu Leu Arg Ser Phe Phe Arg Arg Arg Pro Arg Leu Ser Ser				
266	715	720	725		

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268 acc aac tcc agc agg ttc cca cct tca ccc ctg gct tct aag ccc aca	2562
269 Thr Asn Ser Ser Arg Phe Pro Pro Ser Pro Leu Ala Ser Lys Pro Thr	
270 730 735 740	
272 gtc tca gtg agc atc aac aac ctg tac cca ggc tgc gag aac gtg agt	2610
273 Val Ser Val Ser Ile Asn Asn Leu Tyr Pro Gly Cys Glu Asn Val Ser	
274 745 750 755	
276 gtg agg agc cgc agc atg atg ttc gag ccg ggt ctt acc aaa ggg atg	2658
277 Val Arg Ser Arg Ser Met Met Phe Glu Pro Gly Leu Thr Lys Gly Met	
278 760 765 770	
280 ctg gag gtg ttt gtg gcc ccg acc cac cac ccg cac tgc tcg gcc gat	2706
281 Leu Glu Val Phe Val Ala Pro Thr His His Pro His Cys Ser Ala Asp	
282 775 780 785 790	
284 gac cag tcc acc aag gcc atc gac atc cag aac gct tat ttg aat gga	2754
285 Asp Gln Ser Thr Lys Ala Ile Asp Ile Gln Asn Ala Tyr Leu Asn Gly	
286 795 800 805	
288 gtt ggc gat ttc agc gtg tgg gag ttc tct gga aat cct gtg tat ttc	2802
289 Val Gly Asp Phe Ser Val Trp Glu Phe Ser Gly Asn Pro Val Tyr Phe	
290 810 815 820	
292 tgc tgt tat gac tat ttt gct gca aat gat ccc acg tca atc cat gtt	2850
293 Cys Cys Tyr Asp Tyr Phe Ala Ala Asn Asp Pro Thr Ser Ile His Val	
294 825 830 835	
296 gtt gtc ttt agt ctá gaa gag ccc tat gag atc cag ctg aac cca gtg	2898
297 Val Val Phe Ser Leu Glu Glu Pro Tyr Glu Ile Gln Leu Asn Pro Val	
298 840 845 850	
300 att ttc tgg ctc agt ttc ctg aag tcc ctt gtc cca gtt gaa gaa ccc	2946
301 Ile Phe Trp Leu Ser Phe Leu Lys Ser Leu Val Pro Val Glu Glu Pro	
302 855 860 865 870	
304 ata gcc ttc ggt ggc aag ctg aag aac cca ctc caa gtt gtc ctg gtg	2994
305 Ile Ala Phe Gly Gly Lys Leu Lys Asn Pro Leu Gln Val Val Leu Val	
306 875 880 885	
308 gcc acc cac gct gac atc atg aat gtt cct cga ccg gct gga ggc gag	3042
309 Ala Thr His Ala Asp Ile Met Asn Val Pro Arg Pro Ala Gly Gly Glu	
310 890 895 900	
312 ttt gga tat gac aaa gac aca tcg ttg ctg aaa gag att agg aac agg	3090
313 Phe Gly Tyr Asp Lys Asp Thr Ser Leu Leu Lys Glu Ile Arg Asn Arg	
314 905 910 915	
316 ttt gga aat gat ctt cac att tca aat aag ctg ttt gtt ctg gat gct	3138
317 Phe Gly Asn Asp Leu His Ile Ser Asn Lys Leu Phe Val Leu Asp Ala	
318 920 925 930	
320 ggg gct tct ggg tca aag gac atg aag gta ctt cga aat cat ctg caa	3186
321 Gly Ala Ser Gly Ser Lys Asp Met Lys Val Leu Arg Asn His Leu Gln	
322 935 940 945 950	
324 gaa ata cga agc cag att gtt tcg gtc tgt cct ccc atg act cac ctg	3234
325 Glu Ile Arg Ser Gln Ile Val Ser Val Cys Pro Pro Met Thr His Leu	
326 955 960 965	
328 tgt gag aaa atc atc tcc acg ctg cct tcc tgg agg aag ctc aat gga	3282
329 Cys Glu Lys Ile Ile Ser Thr Leu Pro Ser Trp Arg Lys Leu Asn Gly	
330 970 975 980	
332 ccc aac cag ctg atg tcg ctg cag cag ttt gtg tac gac gtg cag gac	3330

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L:73 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:71
L:882 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:880